APPENDIX A

Genbank Accession # M21616

Sequence of human PDGF receptor seta

TGTTCTCCTGAGCCTTCAGGAGCCTGCACCAGTCCTGCCTG												
AGCTGTTACCCACTCTGGGACCAGCAGTCTTTCTGATAACTGGGAGAGGGCAGTAAGGAGGACTTCC												
TGGAGGGGGTG	ACTGTCCA	GAGCCTGG.	AACTGT	GCCCACA	ACCAGA	AAGCC?	ATCAGCA	GCAA	GGACACC	186		
ATG CGG CTT Met Arg Leu										237 -15		
TTG CTG TCT Leu Leu Ser	CTC CTG	TTA CTT Leu Leu	CTG G	AA CCA lu Pro	CAG F	ATC TO	CT CAG er Gln	GGC Gly	CTG GTC Leu Val	288 2		
GTC ACA CCC										339 19		
CTG ACC TGC Leu Thr Cys										390 36		
CCC CCA CAG Pro Pro Gin										441 53		
ACA CTG ACC										492 70		
AAT GAC TCC Asn Asp Ser										543 87		
GTG CCA GAT Val Pro Asp										594 104		
ATC TTT CTC										645 121		
CCA CAG CTG										696 138		
GTC CCC TAT										747 155		
TAC ATC TGC Tyr Ile Cys										798 172		
TAT GTC TAC										849 189		
CAG ACT GTG										900 206		
GGG AAT GAT Gly Asn Asp												
CGG CTG GTG	GAG CCG	GTG ACT	GAC T	TC CTC he Leu	TTG (GAT A' Asp Me	TG CCT et Pro	TAC Tyr	CAC ATC	1002 240		
CGC TCC ATC	CTG CAC	ATC CCC	AGT G	CC GAG	TTA (GAA G	AC TCG	GGG	ACC TAC	1053		

Arg Ser Ile Leu His Ile Pro Ser Ala Glu Leu Glu Asp Ser Gly Thr Tyr ACC TSC AAT GTG ACG GAG AST STG AAT GAC CAT CAG GAT GAA AAG GCC ATC 1104 Thr Cys Asn Val Thr Glu Ser Val Asn Asp His Gln Asp Glu Lys Ala Ile AAC ATC ACC GTG GTT GAG AGC GGC TAC GTG CGG CTC CTG GGA GAG GTG GGC Asn Ile Thr Val Val Glu Ser Gly Tyr Val Arg Leu Leu Gly Glu Val Gly ACA CTA CAA TIT GCT GAG CTG CAT CGG AGC CGG ACA CTG CAG GTA GTG TTC 1206 Thr Leu Gln Phe Ala Glu Leu His Arg Ser Arg Thr Leu Gln Val Val Phe GAG GCC TAC CCA CCG CCC ACT GTC CTG TGG TTC AAA GAC AAC CGC ACC CTG 1257 Glu Ala Tyr Pro Pro Pro Thr Val Leu Trp Phe Lys Asp Asn Arg Thr Leu GGC GAC TCC AGC GCT GGC GAA ATC GCC CTG TCC ACG CGC AAC GTG TCG GAG 1308 Gly Asp Ser Ser Ala Gly Glu Ile Ala Leu Ser Thr Arg Asn Val Ser Glu ACC CGG TAT GTG TCA GAG CTG ACA CTG GTT CGC GTG AAG GTG GCA GAG GCT 1359 Thr Arg Tyr Val Ser Glu Leu Thr Leu Val Arg Val Lys Val Ala Glu Ala GGC CAC TAC ACC ATG CGG GCC TTC CAT GAG GAT GCT GAG GTC CAG CTC TCC 1410 Gly His Tyr Thr Met Arg Ala Phe His Glu Asp Ala Glu Val Gln Leu Ser TTC CAG CTA CAG ATC AAT GTC CCT GTC CGA GTG CTG GAG CTA AGT GAG AGC 1461 Phe Gln Leu Gln Ile Asn Val Pro Val Arq Val Leu Glu Leu Ser Glu Ser CAC CCT GAC AGT GGG GAA CAG ACA GTC CGC TGT CGT GGC CGG GGC ATG CCG 1512 His Pro Asp Ser Gly Glu Gln Thr Val Arg Cys Arg Gly Arg Gly Met Pro 410 CAG CCG AAC ATC ATC TGG TCT GCC TGC AGA GAC CTC AAA AGG TGT CCA CGT 1563 Gln Pro Asn Ile Ile Trp Ser Ala Cys Arg Asp Leu Lys Arg Cys Pro Arg GAG CTG CCG CCC ACG CTG CTG GGG AAC AGT TCC GAA GAG GAG AGC CAG CTG 1614 Glu Leu Pro Pro Thr Leu Leu Gly Asn Ser Ser Glu Glu Glu Ser Gln Leu GAG ACT AAC GTG ACG TAC TGG GAG GAG GAG GAG TTT GAG GTG GTG AGC 1665 Glu Thr Asn Val Thr Tyr Trp Glu Glu Glu Glu Phe Glu Val Val Ser ACA CTG CGT CTG CAG CAC GTG GAT CGG CCA CTG TCG GTG CGC TGC ACG CTG Thr Leu Arg Leu Gln His Val Asp Arg Pro Leu Ser Val Arg Cys Thr Leu CGC AAC GCT GTG GGC CAG GAC ACG CAG GAG GTC ATC GTG GTG CCA CAC TCC 1767 Arg Asn Ala Val Gly Gln Asp Thr Gln Glu Val Ile Val Val Pro His Ser 495 TTG CCC TTT AAG GTG GTG GTG ATC TCA GCC ATC CTG GCC CTG GTG GTG CTC 1818 Leu Pro Phe Lys Val Val Val Ile Ser Ala Ile Leu Ala Leu Val Val Leu ACC ATC ATC TCC CTT ATC ATC CTC ATC ATG CTT TGG CAG AAG AAG CCA CGT Thr Ile Ile Ser Leu Ile Ile Leu Ile Met Leu Trp Gln Lys Lys Pro Arg 529 TAC GAG ATC CGA TGG AAG GTG ATT GAG TCT GTG AGC TCT GAC GGC CAT GAG 1920 Tyr Glu Ile Arg Trp Lys Val Ile Glu Ser Val Ser Ser Asp Gly His Glu TAC ATC TAC GTG GAC CCC ATG CAG CTG CCC TAT GAC TCC ACG TGG GAG CTG 1971 Tyr Ile Tyr Val Asp Pro Met Gln Leu Pro Tyr Asp Ser Thr Trp Glu Leu COS CGG GAC CAG CTT GTG CTG GGA CGC ACC CTC GGC TCT GGG GCC TTT GGG 2022 Pro Arg Asp Gin Leu Val Leu Gly Arg Thr Leu Gly Ser Gly Ala Phe Gly

CAG GTG GTG GAG GCC ACA GCT CAT GGT CTG AGC CAT TCT CAG GCC ACG ATG 2073 Gin Val Val Glu Ala Thr Ala His Gly Leu Ser His Ser Gln Ala Thr Met AAA GTG GCC GTC AAG ATG CTT AAA TCC ACA GCC CGC AGC AGT GAG AAG CAA 2124 Lys Vai Ala Val Lys Met Leu Lys Ser Thr Ala Arg Ser Ser Glu Lys Gln GCC CTT ATG TOG GAG CTG AAG ATC ATG AGT CAC CTT GGG CCC CAC CTG AAC 2175 Ala Leu Met Ser Glu Leu Lys Ile Met Ser His Leu Gly Pro His Leu Asn 631 GTG GTC AAC CTG TTG GGG GCC TGC ACC AAA GGA GGA CCC ATC TAT ATC ATC 2226 Val Val Asn Leu Leu Gly Ala Cvs Thr Lvs Gly Gly Pro Ile Tyr Ile Ile ACT GAG TAC TGC CGC TAC GGA GAC CTG GTG GAC TAC CTG CAC CGC AAC AAA 2277 Thr Glu Tyr Cys Arg Tyr Gly Asp Leu Val Asp Tyr Leu His Arg Asn Lys 665 CAC ACC TTC CTG CAG CAC CAC TCC GAC AAG CGC CGC CCG CCC AGC GCG GAG His Thr Phe Leu Gln His His Ser Asp Lys Arg Pro Pro Ser Ala Glu CTC TAC AGC AAT GCT CTG CCC GTT GGG CTC CCC CTG CCC AGC CAT GTG TCC 2379 Leu Tyr Ser Asn Ala Leu Pro Val Gly Leu Pro Leu Pro Ser His Val Ser 699 TTG ACC GGG GAG AGC GAC GGT GGC TAC ATG GAC ATG AGC AAG GAC GAG TCG 2430 Leu Thr Gly Glu Ser Asp Gly Gly Tyr Met Asp Met Ser Lys Asp Glu Ser GTG GAC TAT GTG CCC ATG CTG GAC ATG AAA GGA GAC GTC AAA TAT GCA GAC 2481 Val Asp Tyr Val Pro Met Leu Asp Met Lys Gly Asp Val Lys Tyr Ala Asp 733 ATC GAG TCC TCC AAC TAC ATG GCC CCT TAC GAT AAC TAC GTT CCC TCT GCC 2532 Ile Glu Ser Ser Asn Tyr Met Ala Pro Tyr Asp Asn Tyr Val Pro Ser Ala 750 CCT GAG AGG ACC TGC CGA GCA ACT TTG ATC AAC GAG TCT CCA GTG CTA AGC 2583 Pro Glu Arg Thr Cys Arg Ala Thr Leu Ile Asn Glu Ser Pro Val Leu Ser 767 TAC ATG GAC CTC GTG GGC TTC AGC TAC CAG GTG GCC AAT GGC ATG GAG TTT 2634 Tyr Met Asp Leu Val Gly Phe Ser Tyr Gln Val Ala Asn Gly Met Glu Phe 784 CTG GCC TCC AAG AAC TGC GTC CAC AGA GAC CTG GCG GCT AGG AAC GTG CTC 2685 Leu Ala Ser Lys Asn Cys Val His Arg Asp Leu Ala Ala Arg Asn Val Leu 801 ATC TGT GAA GGC AAG CTG GTC AAG ATC TGT GAC TTT GGC CTG GCT CGA GAC 2736 Ile Cys Glu Gly Lys Leu Val Lys Ile Cys Asp Phe Gly Leu Ala Arg Asp ATC ATG CGG GAC TCG AAT TAC ATC TCC AAA GGC AGC ACC TTT TTG CCT TTA 2787 Ile Met Arg Asp Ser Asn Tyr Ile Ser Lys Gly Ser Thr Phe Leu Pro Leu 835 AAG TGG ATG GCT CCG GAG AGC ATC TTC AAC AGC CTC TAC ACC ACC CTG AGC 2838 Lys Trp Met Ala Pro Glu Ser Ile Phe Asn Ser Leu Tyr Thr Thr Leu Ser GAC GTG TGG TCC TTC GGG ATC CTG CTC TGG GAG ATC TTC ACC TTG GGT GGC 2889 Asp Val Trp Ser Phe Gly Ile Leu Leu Trp Glu Ile Phe Thr Leu Gly Gly 869 ACC CCT TAC CCA GAG CTG CCC ATG AAC GAG CAG TTC TAC AAT GCC ATC AAA 2940 Thr Pro Tyr Pro Glu Leu Pro Met Asn Glu Gln Phe Tyr Asn Ala Ile Lys CGG GGT TAC CGC ATG GCC CAG CCT GCC CAT GCC TCC GAC GAG ATC TAT GAG Arg Gly Tyr Arg Met Ala Gln Pro Ala His Ala Ser Asp Glu Ile Tyr Glu

ATC ATG CAG AAG TGC TGG GAA GAG AAG TTT GAG ATT CGG CCC CCC TTC TCC Ile Met Gln Lys Cys Trp Glu Glu Lys Phe Glu Ile Arg Pro Pro Phe Ser CAG CTG GTG CTG CTT CTC GAG AGA CTG TTG GGC GAA GGT TAC AAA AAG AAG 3093 Gin Leu Val Leu Leu Glu Arg Leu Leu Gly Glu Gly Tyr Lys Lys Lys TAC CAG CAG GTG GAT GAG GAG TTT CTG AGG AGT GAC CAC CCA GCC ATC CTT 3144 Tyr Gln Gln Val Asp Glu Glu Phe Leu Arg Ser Asp His Pro Ala Ile Leu 954 CGG TCC CAG GCC CGC TTG CCT GGG TTC CAT GGC CTC CGA TCT CCC CTG GAC 3195 Arg Ser Gln Ala Arg Leu Pro Gly Phe His Gly Leu Arg Ser Pro Leu Asp ACC AGC TCC GTC CTC TAT ACT GCC GTG CAG CCC AAT GAG GGT GAC AAC GAC 988 Thr Ser Ser Val Leu Tyr Thr Ala Val Gln Pro Asn Glu Gly Asp Asn Asp TAT ATC ATC CCC CTG CCT GAC CCC AAA CCT GAG GTT GCT GAC GAG GGC CCA 3297 Tyr Ile Ile Pro Leu Pro Asp Pro Lys Pro Glu Val Ala Asp Glu Gly Pro 1005 CTG GAG GGT TCC CCC AGC CTA GCC AGC TCC ACC CTG AAT GAA GTC AAC ACC 3348 Leu Glu Gly Ser Pro Ser Leu Ala Ser Ser Thr Leu Asn Glu Val Asn Thr 1022 TCC TCA ACC ATC TCC TGT GAC AGC CCC CTG GAG CCC CAG GAC GAA CCA GAG 3399 Ser Ser Thr Ile Ser Cys Asp Ser Pro Leu Glu Pro Gln Asp Glu Pro Glu 1039 CCA GAG CCC CAG CTT GAG CTC CAG GTG GAG CCG GAG CCG GAG CTG GAA CAG 3450 Pro Glu Pro Gln Leu Glu Leu Gln Val Glu Pro Glu Pro Glu Leu Glu Gln 1056 TTG CCG GAT TCG GGG TGC CCT GCG CCT CGG GCG GAA GCA GAG GAT AGC TTC Leu Pro Asp Ser Gly Cys Pro Ala Pro Arg Ala Glu Ala Glu Asp Ser Phe 1073 CTG TAGGGGGCTGGCCCTACCCTGCCTGAAGCTCCCCGCTGCCAGCACCCAGCATCTCC 3567 Leu 1074 TGGCCTGGCCTGGCCGGGCTTCCTGTCAGCCAGGCTGCCCTTATCAGCTGTCCCCTTCTGGAAGCTT 3634 TCTGCTCCTGACGTGTTGTGCCCCAAACCCTGGGGTGGCTTAGGAGGCAAGAAAACTGCAGGGGCC GTGACCAGCCCTCTGCCTCCAGGGAGGCCAACTGACTCTGAGCCAGGGTTCCCCCAGGGAACTCAGT 3768 TTTCCCATATGTAAGATGGGAAAGTTAGGCTTGATGACCCAGAATCTAGGATTCTCTCCCTGGCTGA 3835 CAGGTGGGGAGACCGAATCCCTCCCTGGGAAGATTCTTGGAGTTACTGAGGTGGTAAATTAACTTTT 3902 TTCTGTTCAGCCAGCTACCCCTCAAGGAATCATAGCTCTCCTCGCACTTTTATCCACCCAGGAGC 3969 TAGGGAAGAGACCCTAGCCTCCCTGGCTGGCTGAGCTAGGCCTAGCCTTGAGCAGTGTTGCCT 4036 CATCCAGAAGAAAGCCAGTCTCCTCCTATGATGCCAGTCCCTGCGTTCCCTGGCCCGAGCTGGTCT 4103 GGGCCATTAGGCAGCCTAATTAATGCTGGAGGCTGAGCCAAGTACAGGACACCCCCAGCCTGCAGC 4170 CCTTGCCCAGGGCACTTGGAGCACACGCAGCCATAGCAAGTGCCTGTGCCTGTCCTTCAGGCCCA 4237 4304 4371 ATGGCCCTGGCTCTGCACTGCTATGAGGCTTTGGAGGAATCCCTCACCCTCTCTGGGCCTC 4438

(4)

AGTTTCCCCTTCAAAAAATGAATAAGTCGGACTTATTAACTCTGAGTGCCTTGCCAGCACTAACATT	4505
CTAGAGTATCCAGGTGGTTGCACATTTGTCCAGATGAAGCAAGGCCATATACCCTAAACTTCCATCC	4572
TGGGGGTCAGCTGGGCTCCTGGGAGATTCCAGATCACACATCACACTCTGGGGACTCAGGAACCATG	4639
CCCTTCCCCAGGCCCCAGCAAGTCTCAAGAACACAGCTGCACAGGCCTTGACTTAGAGTGACAGC	4706
CGGTGTCCTGGAAAGCCCCCAGCAGCTGCCCCAGGGACATGGGAAGACCACGGGACCTCTTTCACTA	4773
CCACGATGACCTCCGGGGTATCCTGGGCAAAAGGGGACAAAGAGGGCAAATGAGATCACCTCCTGC	4840
AGCCCACCACTCCAGCACCTGTGCCGAGGTCTGCGTCGAAGACAGAATGGACAGTGAGGACAGTTAT	4907
GTCTTGTAAAAGACAAGAAGCTTCAGATGGGTACCCCAAGAAGGATGTGAGAGGTGGGCGCTTTGGA	4974
GGTTTGCCCCTCACCCACCAGCTGCCCCATCCCTGAGGCAGCGCTCCATGGGGGTATGGTTTGTCA	5041
CTGCCCAGACCTAGCAGTGACATCTCATTGTCCCCAGCCCAGTGGGCATTGGAGGTGCCAGGGGAGT	5108
CAGGGTTGTAGCCAAGACGCCCCCCCCACGGGGAGGGTTGGGAAGGGGGTGCAGGAAGCTCAACCCCT	517
CTGGGCACCAACCCTGCATTGCAGGTTGGCACCTTACTTCCCTGGGATCCCAGAGTTGGTCCAAGGA	5242
GGGAGAGTGGGTTCTCAATACGGTACCAAAGATATAATCACCTAGGTTTACAAATATTTTTAGGACT	530
CACGTTAACTCACATTTATACAGCAGAAATGCTATTTTGTATGCTGTTAAGTTTTTCTATCTGTGTA	537
CTTTTTTTTAAGGGAAAGATTTTAATATTAAACCTGGTGCTTCTCACTCA	542

Sequence of human PDGF receptor alpha

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	TTGGAGCTACAGGGAGAAACAGAGGAGGAGACTGCAAGAGATCATTGGAGGCCGTGGGC													GGC	61		
ACG	ACGCTCTTTACTCCATGTGTGGGACATTCATTGCGGAATAACATCGGAGGAGAAGTTTCCCAGAGCT														GCT	128	
										TTA Leu							179 -7
CTG Leu	AGC Ser	CTA Leu	ATC Ile	CTC Leu	TGC Cys	CAG Gln	CTT Leu	TCA Ser	TTA Leu	CCC Pro	TCT Ser	ATC Ile	CTT Leu	CCA Pro	AAT Asn	GAA Glu	230 11
										TTT Phe							281 28
										TCT Ser							332 45
										GGC Gly							383 62
										GGG Gly							434 79
										GAA Glu							485 96
										CCT Pro							536 113
										ATT Ile							587 130
										AGT Ser							638 147
										ACC Thr							689 164
										TTC Phe							7 40 181
										GAT Asp							791 198
										GTG Val							842 215
AAC Asn	AAT Asn	GAG Glu	GTG Val	GTT Val	GAC Asp	CTT Leu	CAA Gln	TGG Trp	ACT Thr	TAC Tyr	CCT Pro	GGA Gly	GAA Glu	GTG Val	AAA Lys	GGC Gly	8 93 2 32
										GTC Val							944 24 9
TAC Tyr	ACT Thr	TTG Leu	ACG Thr	GTC Val	CCC Pro	GAG Glu	GCC Ala	ACG Thr	GTG Val	LVa	GAC Asp	AGT Ser	GGA Gly	GAT Asp	TAC Tyr	GAA Glu	995 266

												ATG Met					1046 283
												CCC Pro					1097 300
												GTT Val					1148 317
												AAT Asn					1199 334
GAA	AAT	CTC	ACT	GAG	ATC	ACC	ACT	GAT	GTG	GAA	AAG	ATT	CAG	GAA	ATA	AGG	1250
								•			-	Ile GAA				_	351 1301
Tyr	Arg	Ser	Lys	Leu	Lys	Leu	Ile	Arg	Ala	Lys	Glu	Glu	Asp	Ser	Gly	His	368
												AGC Ser					135 2 385
												GTC Val					1403 402
												GAA Glu					1454 419
CCT	GAT	ATT	GAG	TGG	ATG	ATA	TGC	AAA	GAT	ATT	AAG	AAA	TGT	AÁT	AAT	GAA	1505
Pro	Asp	Ile	Glu	Trp	Met	Ile	Суз	Lys	Asp	Ile	Lys	Lys	Суз	Asn	Asn	Glu	436
												ATC Ile					1556 453
												ACT Thr					1607 470
												CTC					1658
						-	_			-		Leu		_			487
												TCT Ser					1709 504
												ATC Ile					1760 521
CTG Leu	GTT Val	GTC Val	ATT Ile	TGG Trp	AAA eyl	CAG Gln	AAA Lys	CCG Pro	AGG Arg	TAT Tyr	GAA Glu	ATT Ile	CGC Arg	TGG Trp	AGG Arg	GTC Val	1811 538
												TAT Tyr					1862 555
												GAT Asp					1913 572
GGT	CGG	GTC	TTG	GGG	TCT	GGA	GCG	TTŢ	GGG	AAG	GTG	GTT Val	GAA	GGA	ACA	GCC	1964 589
						-			_	-				_			

TAT GGA TTA AGC CGG TCC CAA CCT GTC ATG AAA GTT GCA GTG AAG ATG CTA Tyr Gly Leu Ser Arg Ser Gln Pro Val Met Lys Val Ala Val Lys Met Leu AAA CCC ACG GCC AGA TCC AGT GAA AAA CAA GCT CTC ATG TCT GAA CTG AAG Lys Pro Thr Ala Arg Ser Ser Glu Lys Gln Ala Leu Met Ser Glu Leu Lys ATA ATG ACT CAC CTG GGG CCA CAT TTG AAC ATT GTA AAC TTG CTG GGA GCC 2117 Ile Met Thr His Leu Gly Pro His Leu Asn Ile Val Asn Leu Leu Gly Ala TGC ACC AAG TCA GGC CCC ATT TAC ATC ACA GAG TAT TGC TTC TAT GGA 2168 Cys Thr Lys Ser Gly Pro Ile Tyr Ile Ile Thr Glu Tyr Cys Phe Tyr Gly 657 GAT TTG GTC AAC TAT TTG CAT AAG AAT AGG GAT AGC TTC CTG AGC CAC CAC 2219 Asp Leu Val Asn Tyr Leu His Lys Asn Arg Asp Ser Phe Leu Ser His His CCA GAG AAG CCA AAG AAA GAG CTG GAT ATC TTT GGA TTG AAC CCT GCT GAT 2270 Pro Glu Lys Pro Lys Lys Glu Leu Asp Ile Phe Gly Leu Asn Pro Ala Asp 691 GAA AGC ACA CGG AGC TAT GTT ATT TTA TCT TTT GAA AAC AAT GGT GAC TAC 2321 Glu Ser Thr Arg Ser Tyr Val Ile Leu Ser Phe Glu Asn Asn Gly Asp Tyr ATG GAC ATG AAG CAG GCT GAT ACT ACA CAG TAT GTC CCC ATG CTA GAA AGG 2372 Met Asp Met Lys Gln Ala Asp Thr Thr Gln Tyr Val Pro Met Leu Glu Arg AAA GAG GTT TCT AAA TAT TCC GAC ATC CAG AGA TCA CTC TAT GAT CGT CCA 2423 Lys Glu Val Ser Lys Tyr Ser Asp Ile Gln Arg Ser Leu Tyr Asp Arg Pro GCC TCA TAT AAG AAG AAA TCT ATG TTA GAC TCA GAA GTC AAA AAC CTC CTT 2474 Ala Ser Tyr Lys Lys Lys Ser Met Leu Asp Ser Glu Val Lys Asn Leu Leu TCA GAT GAT AAC TCA GAA GGC CTT ACT TTA TTG GAT TTG TTG AGC TTC ACC 2525 Ser Asp Asp Asn Ser Glu Gly Leu Thr Leu Leu Asp Leu Leu Ser Phe Thr 776 TAT CAA GTT GCC CGA GGA ATG GAG TTT TTG GCT TCA AAA AAT TGT GTC CAC 2576 Tyr Gln Val Ala Arg Gly Met Glu Phe Leu Ala Ser Lys Asn Cys Val His CGT GAT CTG GCT GCT CGC AAC GTT CTC CTG GCA CAA GGA AAA ATT GTG AAG 2627 Arg Asp Leu Ala Ala Arg Asn Val Leu Leu Ala Gln Gly Lys Ile Val Lys ATC TGT GAC TTT GGC CTG GCC AGA GAC ATC ATG CAT GAT TCG AAC TAT GTG 2678 Ile Cys Asp Phe Gly Leu Ala Arg Asp Ile Met His Asp Ser Asn Tyr Val TCG AAA GGC AGT ACC TTT CTG CCC GTG AAG TGG ATG GCT CCT GAG AGC ATC 2729 Ser Lys Gly Ser Thr Phe Leu Pro Val Lys Trp Met Ala Pro Glu Ser Ile TTT GAC AAC CTC TAC ACC ACA CTG AGT GAT GTC TGG TCT TAT GGC ATT CTG 2780 Phe Asp Asn Leu Tyr Thr Thr Leu Ser Asp Val Trp Ser Tyr Gly Ile Leu 861 CTC TGG GAG ATC TTT TCC CTT GGT GGC ACC CCT TAC CCC GGC ATG ATG GTG 2831 Leu Trp Glu Ile Phe Ser Leu Gly Gly Thr Pro Tyr Pro Gly Met Met Val GAT TCT ACT TTC TAC AAT AAG ATC AAG AGT GGG TAC CGG ATG GCC AAG CCT Asp Ser Thr Phe Tyr Asn Lys Ile Lys Ser Gly Tyr Arg Met Ala Lys Pro-GAC CAC GCT ACC AGT GAA GTC TAC GAG ATC ATG GTG AAA TGC TGG AAC AGT Asp His Ala Thr Ser Glu Val Tyr Glu Ile Met Val Lys Cys Trp Asn Ser

(3)

GAG CCG GAG AAG AGA CCC TCC TTT TAC CAC CTG AGT GAG ATT GTG GAG AAT Glu Pro Glu Lys Arg Pro Ser Phe Tyr His Leu Ser Glu Ile Val Glu Asn CTG CTG CCT GGA CAA TAT AAA AAG AGT TAT GAA AAA ATT CAC CTG GAC TTC 3035 Leu Leu Pro Gly Gln Tyr Lys Lys Ser Tyr Glu Lys Ile His Leu Asp Phe CTG AAG AGT GAC CAT CCT GCT GTG GCA CGC ATG CGT GTG GAC TCA GAC AAT 3086 Leu Lys Ser Asp His Pro Ala Val Ala Arg Met Arg Val Asp Ser Asp Asn GCA TAC ATT GGT GTC ACC TAC AAA AAC GAG GAA GAC AAG CTG AAG GAC TGG 3137 Ala Tyr Ile Gly Val Thr Tyr Lys Asn Glu Glu Asp Lys Leu Lys Asp Trp 980 GAG GGT GGT CTG GAT GAG CAG AGA CTG AGC GCT GAC AGT GGC TAC ATC ATT 3188 Glu Gly Gly Leu Asp Glu Gln Arg Leu Ser Ala Asp Ser Gly Tyr Ile Ile CCT CTG CCT GAC ATT GAC CCT GTC CCT GAG GAG GAG GAC CTG GGC AAG AGG 3239 Pro Leu Pro Asp Ile Asp Pro Val Pro Glu Glu Glu Asp Leu Gly Lys Arg 1014 AAC AGA CAC AGC TCG CAG ACC TCT GAA GAG AGT GCC ATT GAG ACG GGT TCC 3290 Asn Arg His Ser Ser Gln Thr Ser Glu Glu Ser Ala Ile Glu Thr Gly Ser 1031 AGC AGT TCC ACC TTC ATC AAG AGA GAG GAC GAG ACC ATT GAA GAC ATC GAC Ser Ser Ser Thr Phe Ile Lys Arg Glu Asp Glu Thr Ile Glu Asp Ile Asp ATG ATG GAC GAC ATC GGC ATA GAC TCT TCA GAC CTG GTG GAA GAC AGC TTC 3392 Met Met Asp Asp Ile Gly Ile Asp Ser Ser Asp Leu Val Glu Asp Ser Phe CTG TAACTGGCGGATTCGAGGGGTTCCTTCCACTTCTGGGGCCCACCTCTGGATCCCGTTCAGAAAA 3458 1066 CCACTTTATTGCAATGCGGAGGTTGAGAGGAGGACTTGGTTGATGTTTAAAGAGAAGTTCCCAGCCA 3525 AGGGCCTCGGGGAGCCTTTCTAAATATGAATGAATGGGATATTTTGAAATGAACTTTGTCAGTGTTG 3592 ATAGGCCACAGAAGGTGAACTTTCTGCTTCAAGGACATTGGTGAGAGTCCAACAGACACAATTTATA 3726 CTGCGACAGAACTTCAGCATTGTAATTATGTAAATAACTCTAACCACGGCTGTGTTTAGATTGTATT 3860 3927 TGTCAGCTGCTGTTGAACTTTTTAAAGAAGTGCATGAAAAACCATTTTTGACCTTAAAAGGTACTGG 3994 TAATAGATTTGGGTCATTTAGAAGCCTGACAACTCATTTTCATATTGTAATCTATGTTATAATACT 4061 ACTACTGTTATCAGTAATGCTAAATGTGTAATAATGTAACATGATTTCCCTCCACACAAAGCACAAT 4128 TTAAAAACAATCCTTACTAAGTAGGTGATGAGTTTGACAGTTTTTGACATTTATATTAAATAACATG 4195 TTTCTCTATAAAGTATGGTAATAGCTTTAGTGAATTAAATTTAGTTGAGCATAGAGAACAAAGTAAA AGTAGTGTTGTCCAGGAAGTCAGAATTTTTAACTGTACTGAATAGGTTCCCCAATCCATCGTATTAA 4329 CTCAATGTAGAGGCATAAACCTGTGCTGAACATAACTTCTCATGTATATTACCCAATGGAAAATATA 4463 4530 TTTGGCGACCCCAATATATGTATTTTTTGAATCTATGAACCTGAAAAGGGTCACAAAGGATGCCCAG 4597 ACATCAGCCTCCTTCTTCACCCCTTACCCCAAAGAGAAAGAGTTTGAAACTCGAGACCATAAAGAT 4664 4731 TAGACTAGTACCTGGGTTTCCATCCTTGAGATTCTGAAGTATGAAGTCTGAGGGGAAACCAGAGTCTG 4798 TATTTTTCTAAACTCCCTGGCTGTTCTGATCGGCCAGGTTTCGGAAACACTGACTTAGGTTTCAGGA 4865 AGTTGCCATGGGAAACAATAATTTGAACTTTGGAACAGGGTTCTTAAGTTGGTGCGTCCTTCGGAT 4932 AATTGAAAGGTCAGAATCGACTCCTTTCGATTTCAAACCAAAACTGTCCAAAAGGTTTTCAT 5066 TTCTACGATGAAGGGTGACATACCCCCTCTAACTTGAAAGGGGCAGAGGGCAGAAGAGCGGAGGGTG 5133 AGGTATGGGGCGGTTCCTTTCCGTACATGTTTTTAATACGTTAAGTCACAAGGTTCAGAGACACATT GGTCGAGTCACAAAACCACCTTTTTTGTAAAATTCAAAATGACTATTAAACTCCAATCTACCCTCCT 5267 ACTTAACAGTGTAGATAGGTGTGACAGTTTGTCCAACCACACCACAGTAACCGTAAGAAACGTTATG 5334 ACGAATTAACGACTATGGTATACTTACTTTGTACCCGACACTAATGACGTTAGTGACACGATAGCCG 5401 CGTTCGGGGTTGAAAGAATAGGTTGAAAAAGTATCATTCACGCTTCTGACTCGGTCTAACCGGTTAA 5535 TTTTTCTTTTGGACTGATCCAAGACATCTCGGTTAATCTGAACTTTATGCAAACACAAAGATCTTAG 5602 TGTCGAGTTCGTAAGACAAATAGCGAGTGAGAGGGAACATGTCGGAATAAAACAACCACGAAACGTA 5669 AAACTATAACGACACTCGGAACGTACTGTAGTACTCCGGCCTACTTTGAAGAGTCAGGTCGTCAAAG 5736 CGTTTAAGGTCTAAACAAAGGAAAACCGGAGGACGTTTCAGAGGTCTTCTTTAAACGGTTAGAAAG. 5870 GATGAAAGATAAAAATACTACTGTTAGTTTCGGCCGGACTCTTTGTGATAAACACTGAAAAATTTGC 5937 TAATCACTACAGGAATTTTACACCAGACGGTTAGACATGTTTTACCAGGATAAAAACACTTCTCCCT 6071 GTATTCTATTTTACTACAATATGTAGTTATACATATACATAAAGATATATCTGAACCTCTTATGA CGGTTTTGTAAATACTGTTCGACATAGTGACGGAAGCAAATATAAAAAAATTGACACTATTAGGGGT TTATGTTTTACATAATGCTTACGGGGACAAGTACAAAAACAAAATTTTGCACATTTACTTCTAGAAA 6339